


Distance tree of results ~~NEW~~

Sequences producing significant alignments:			Score (Bits)	E Value
gi 157070719 gb EAA28794.2 	hypothetical protein NCU09115 [Neuro		29.5	25
gi 85089616 ref XP_958030.1 	hypothetical protein [Neurospora cr		29.5	25
gi 145517869 ref XP_001444812.1 	hypothetical protein [Parame...		29.1	34
gi 146296177 ref YP_001179948.1 	Allergen V5/Tpx-1 family pro...		28.6	46
gi 66804519 ref XP_635992.1 	hypothetical protein DDBDRAFT_01...		28.6	46
gi 60681778 ref YP_211922.1 	hypothetical protein BF2300 [Bac...		28.2	61
gi 15614366 ref NP_242669.1 	hypothetical protein BH1803 [Bac...		28.2	61
gi 89097516 ref ZP_01170405.1 	hypothetical protein B14911_27...		28.2	61
gi 156977941 ref YP_001448847.1 	hypothetical protein VIBHAR_...		27.8	82
gi 153940849 ref YP_001391336.1 	SCP-like extracellular prote...		27.8	82
gi 149181592 ref ZP_01860086.1 	hypothetical protein BSG1_137...		27.8	82
gi 149179719 ref ZP_01858224.1 	hypothetical protein BSG1_018...		27.8	82
gi 149182265 ref ZP_01860745.1 	hypothetical protein BSG1_199...		27.8	82
gi 148379973 ref YP_001254514.1 	exported protein [Clostridiu...		27.8	82
gi 126651239 ref ZP_01723449.1 	hypothetical protein BB14905_...		27.8	82
gi 91228096 ref ZP_01262138.1 	arginine decarboxylase [Vibrio...		27.8	82
gi 27365676 ref NP_761204.1 	Biosynthetic arginine decarboxyl...		27.8	82
gi 28211946 ref NP_782890.1 	transporter [Clostridium tetani ...		27.8	82
gi 48474851 sp Q8DA54 SPEA VIBVU	Biosynthetic arginine decarboxy		27.8	82
gi 37680170 ref NP_934779.1 	arginine decarboxylase [Vibrio v...		27.8	82
gi 28900025 ref NP_799680.1 	arginine decarboxylase [Vibrio p...		27.8	82
gi 13507984 ref NP_109933.1 	peptide deformylase [Mycoplasma ...		27.8	82
gi 23098322 ref NP_691788.1 	hypothetical protein OB0867 [Oce...		27.8	82
gi 89097558 ref ZP_01170447.1 	hypothetical protein B14911_28...		27.8	82
gi 89097846 ref ZP_01170733.1 	Ykwd [Bacillus sp. NRRL B-1491...		27.8	82
gi 116183343 ref ZP_01473359.1 	hypothetical protein VEx2w_02...		27.8	82
gi 125972821 ref YP_001036731.1 	Allergen V5/Tpx-1 related [C...		27.8	82
gi 120435753 ref YP_861439.1 	cbb3-type cytochrome c oxidase ...		27.4	110
gi 46139389 ref XP_391385.1 	hypothetical protein FG11209.1 [Gib		27.4	110
gi 111064208 gb EAT85328.1 	hypothetical protein SNOG_07862 [Pha		26.9	148
gi 83643746 ref YP_432181.1 	predicted membrane protein [Hahe...		26.9	148
gi 118602457 ref YP_903672.1 	TIM-barrel protein, yjbN family...		26.5	198
gi 118396171 ref XP_001030428.1 	ABC transporter family prote...		26.5	198
gi 71282430 ref YP_269817.1 	hypothetical protein CPS_3120 [C...		26.5	198
gi 27377860 ref NP_769389.1 	probable C4-dicarboxylate-bindin...		26.5	198
gi 89072907 ref ZP_01159464.1 	acylamino-acid-releasing enzym...		26.5	198
gi 145580745 gb ABP87526.1 	NADH dehydrogenase subunit 2 [Ano...		26.1	266
gi 153893299 ref ZP_02014054.1 	hypothetical protein ObacDRAF...		26.1	266
gi 78127855 gb ABB22239.1 	thymidine kinase-like protein [Ovine		26.1	266
gi 83642858 ref YP_438145.1 	ORF21 [Ovine herpesvirus 2] >gi ...		26.1	266
gi 156866610 gb EDO59982.1 	hypothetical protein CLOLEP_02799 [C		25.7	356
gi 155368551 emb CAM98568.1 	NADH4 protein [Ailuropoda melanoлеu		25.7	356
gi 151942736 gb EDN61082.1 	multidrug transporter [Saccharomyces		25.7	356
gi 148298641 ref YP_001249293.1 	NADH dehydrogenase subunit 4...		25.7	356
gi 119859347 ref ZP_01640763.1 	peptidase S9, prolyl oligopep...		25.7	356
gi 118574743 sp P0C262 YCF1B_PIPCE	Putative membrane protein ycf		25.7	356
gi 118081874 ref XP_415358.2 	PREDICTED: similar to SBF1 protein		25.7	356

>gi|157070719|gb|EAA28794.2| hypothetical protein NCU09115 [Neurospora crassa OR7
Length=536



Score = 29.5 bits (62), Expect = 25
Identities = 9/17 (52%), Positives = 11/17 (64%), Gaps = 5/17 (29%)

Query 1 KNVQYWTQMF-----YT 12
KN+Q+W QMF YT
Sbjct 74 KNLQFWQQMFRSIGGYT 90

>gi|85089616|ref|XP_958030.1|  hypothetical protein [Neurospora crassa OR74A]
Length=485


Score = 29.5 bits (62), Expect = 25
Identities = 9/17 (52%), Positives = 11/17 (64%), Gaps = 5/17 (29%)


Query 1 KNVQYWTQMF-----YT 12
KN+Q+W QMF YT
Sbjct 30 KNLQFWQQMFRSIGGYT 46

>gi|145517869|ref|XP_001444812.1|  hypothetical protein [Paramecium tetraurelia]
gi|124412245|emb|CAK77415.1|  unnamed protein product [Paramecium tetraurelia]
Length=1312

Score = 29.1 bits (61), Expect = 34
Identities = 9/12 (75%), Positives = 9/12 (75%), Gaps = 1/12 (8%)


Query 2 NVQY-WTQMFYT 12
NVQY TQM YT
Sbjct 247 NVQYDRTQMLYT 258


>gi|146296177|ref|YP_001179948.1|  Allergen V5/Tpx-1 family protein [Caldicellu
DSM 8903]

gi|145409753|gb|ABP66757.1|  Allergen V5/Tpx-1 family protein [Caldicellulosir
DSM 8903]
Length=203

Score = 28.6 bits (60), Expect = 46
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)



Query 3 VQYWTQMF 10
V YWTQMF
Sbjct 192 VLYWTQMF 199

>gi|66804519|ref|XP_635992.1|  hypothetical protein DDBDRAFT_0188654 [Dictyostel
AX4]

gi|60464332|gb|EAL62481.1|  hypothetical protein DDBDRAFT_0188654 [Dictyosteliu
AX4]
Length=871

Score = 28.6 bits (60), Expect = 46
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 4 QYWTQMFY 11
QYW +MFY
Sbjct 247 QYWNEMFY 254

>gi|60681778|ref|YP_211922.1|  hypothetical protein BF2300 [Bacteroides fragilis
gi|60493212|emb|CAH07994.1|  putative membrane protein [Bacteroides fragilis NC
Length=166

Score = 28.2 bits (59), Expect = 61

Distance tree of results ~~NEW~~

Sequences producing significant alignments:			Score (Bits)	E Value
gi 20026648 ref NP_612690.1 	tegument protein UL47 [Chimpanze...		29.1	34
gi 157353561 emb CAO46078.1 	unnamed protein product [Vitis vini		28.2	61
gi 17543636 ref NP_502415.1 	Y55D9A.2b [Caenorhabditis elegan...		27.8	82
gi 17543634 ref NP_502414.1 	Y55D9A.2a [Caenorhabditis elegan...		27.8	82
gi 154283619 ref XP_001542605.1 	predicted protein [Ajellomyc...		27.4	110
gi 23098322 ref NP_691788.1 	hypothetical protein OB0867 [Oce...		26.9	148
gi 156367217 ref XP_001627315.1 	predicted protein [Nematoste...		26.1	266
gi 120610775 ref YP_970453.1 	Sterol desaturase [Acidovorax a...		26.1	266
gi 29830538 ref NP_825172.1 	hypothetical protein SAV3995 [St...		26.1	266
gi 71282430 ref YP_269817.1 	hypothetical protein CPS_3120 [C...		26.1	266
gi 60680990 ref YP_211134.1 	putative conserved protein found...		26.1	266
gi 37522897 ref NP_926274.1 	magnesium protoporphyrin IX chel...		26.1	266
gi 116201089 ref XP_001226356.1 	hypothetical protein CHGG_08...		26.1	266
gi 66804519 ref XP_635992.1 	hypothetical protein DDBDRAFT_01...		26.1	266
gi 157018437 gb EAL41048.3 	AGAP010349-PA [Anopheles gambiae str		25.7	356
gi 156546066 ref XP_001600764.1 	PREDICTED: similar to conser...		25.7	356
gi 146090941 ref XP_001466400.1 	hypothetical protein LinJ27....		25.7	356
gi 118574743 sp P0C262 YCF1B PIPCE	Putative membrane protein ycf		25.7	356
gi 120436080 ref YP_861766.1 	hypothetical protein GFO_1729 [...		25.7	356
gi 116872625 ref YP_849406.1 	hypothetical protein lwe1209 [L...		25.7	356
gi 118781666 ref XP_559110.2 	ENSANGP00000027759 [Anopheles gamb		25.7	356
gi 110778133 ref XP_623923.2 	PREDICTED: similar to CG32415-PA [25.7	356
gi 157127035 ref XP_001654771.1 	conserved hypothetical prote...		25.7	356
gi 89891610 ref ZP_01203114.1 	conserved hypothetical protein...		25.7	356
gi 60678205 gb AAX33609.1 	AT16442p [Drosophila melanogaster]		25.7	356
gi 85857820 gb ABC86444.1 	IP06113p [Drosophila melanogaster]		25.7	356
gi 83319321 ref YP_424277.1 	hypothetical protein MCAP_0291 [...		25.7	356
gi 73544475 ref XP_848132.1 	hypothetical protein LMJ_0437 [L...		25.7	356
gi 66550872 ref XP_625047.1 	PREDICTED: similar to CG32415-PA [A		25.7	356
gi 24658735 ref NP_729102.1 	CG32415-PA [Drosophila melanogas...		25.7	356
gi 146296177 ref YP_001179948.1 	Allergen V5/Tpx-1 family pro...		25.7	356
gi 125977358 ref XP_001352712.1 	GA16887-PA [Drosophila pseud...		25.7	356
gi 85091947 ref XP_959151.1 	hypothetical protein [Neurospora...		25.7	356
gi 157338152 emb CAO39196.1 	unnamed protein product [Vitis vini		25.2	478
gi 119613126 gb EAW92720.1 	hCG2039071 [Homo sapiens]		25.2	478
gi 113415529 ref XP_001128848.1 	PREDICTED: hypothetical prot...		25.2	478
gi 50419157 ref XP_458101.1 	hypothetical protein DEHA0C10604...		25.2	478
gi 9633831 ref NP_051909.1 	gp020L [Rabbit fibroma virus] >gi...		25.2	478
gi 86372229 gb ABC95175.1 	hypothetical protein [Bacillus thu...		25.2	478
gi 83647025 ref YP_435460.1 	ABC-type amino acid transport/si...		25.2	478
gi 62180772 ref YP_217189.1 	putative inner membrane protein ...		25.2	478
gi 56412901 ref YP_149976.1 	hypothetical protein SPA0666 [Sa...		25.2	478
gi 9633656 ref NP_051734.1 	m20L [Myxoma virus] >gi 6523875 g...		25.2	478

gi 24654051 ref NP_725536.1 	CG8433-PB, isoform B [Drosophila...	24.4	861
gi 19115868 ref NP_594956.1 	hypothetical protein SPAC4D7.03 ...	24.4	861
gi 89072780 ref ZP_01159337.1 	xylose-proton symport [Photoba...	24.4	861
gi 71416344 ref XP_810207.1 	hypothetical protein Tc00.104705...	24.4	861
gi 125807793 ref XP_001360522.1 	GA17244-PA [Drosophila pseud...	24.4	861
gi 85109635 ref XP_963013.1 	hypothetical protein [Neurospora...	24.4	861
gi 154276406 ref XP_001539048.1 	predicted protein [Ajellomyc...	24.0	1155

Alignments

>[gi|20026648|ref|NP_612690.1|](#) **G** tegument protein UL47 [Chimpanzee cytomegalovirus
[gi|19881076|gb|AAM00696.1|AF480884_48](#) **G** tegument protein UL47 [chimpanzee cytome
Length=982

Score = 29.1 bits (61), Expect = 34
Identities = 9/13 (69%), Positives = 9/13 (69%), Gaps = 2/13 (15%)

Query 2 HVQYW--THMFYT 12
HV YW T MFYT
Sbjct 210 HVTYWACTLMFYT 222

>[gi|157353561|emb|CAO46078.1|](#) unnamed protein product [Vitis vinifera]
Length=300

Score = 28.2 bits (59), Expect = 61
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 6 WTHMFY 11
WTHMFY
Sbjct 89 WTHMFY 94

>[gi|17543636|ref|NP_502415.1|](#) **UG** Y55D9A.2b [Caenorhabditis elegans]
[gi|15718325|emb|CAA21703.2|](#) **G** Hypothetical protein Y55D9A.2b [Caenorhabditis ele
Length=511

Score = 27.8 bits (58), Expect = 82
Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 4 QYWTH---MFY 11
QYW+H MFY
Sbjct 32 QYWSHEHGMFY 42

>[gi|17543634|ref|NP_502414.1|](#) **UG** Y55D9A.2a [Caenorhabditis elegans]
[gi|15718326|emb|CAA21702.2|](#) **G** Hypothetical protein Y55D9A.2a [Caenorhabditis ele
Length=502

Score = 27.8 bits (58), Expect = 82
Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 4 QYWTH---MFY 11
QYW+H MFY
Sbjct 32 QYWSHEHGMFY 42

>[gi|154283619|ref|XP_001542605.1|](#) **G** predicted protein [Ajellomyces capsulatus NAM
[gi|150410785|gb|EDN06173.1|](#) **G** predicted protein [Ajellomyces capsulatus NAM1]
Length=239

Score = 27.4 bits (57), Expect = 110

BLAST SEARCH



SEQ ID #20

Distance tree of results ~~NEW~~

Sequences producing significant alignments:		Score (Bits)	E Value
gi 15614366 ref NP_242669.1 	hypothetical protein BH1803 [Bac...	31.6	5.8
gi 89097516 ref ZP_01170405.1 	hypothetical protein B14911_27...	31.6	5.8
gi 46139389 ref XP_391385.1 	hypothetical protein FG11209.1 [Gib	30.8	10
gi 23098322 ref NP_691788.1 	hypothetical protein OB0867 [Oce...	29.5	25
gi 89097846 ref ZP_01170733.1 	Ykwd [Bacillus sp. NRRL B-1491...	29.5	25
gi 13507984 ref NP_109933.1 	peptide deformylase [Mycoplasma ...	28.6	46
gi 154276406 ref XP_001539048.1 	predicted protein [Ajellomyc...	28.2	61
gi 146296177 ref YP_001179948.1 	Allergen V5/Tpx-1 family pro...	28.2	61
gi 156977941 ref YP_001448847.1 	hypothetical protein VIBHAR...	27.8	82
gi 153940849 ref YP_001391336.1 	SCP-like extracellular prote...	27.8	82
gi 149181592 ref ZP_01860086.1 	hypothetical protein BSG1_137...	27.8	82
gi 149179719 ref ZP_01858224.1 	hypothetical protein BSG1_018...	27.8	82
gi 149182265 ref ZP_01860745.1 	hypothetical protein BSG1_199...	27.8	82
gi 148379973 ref YP_001254514.1 	exported protein [Clostridiu...	27.8	82
gi 126651239 ref ZP_01723449.1 	hypothetical protein BB14905...	27.8	82
gi 91228096 ref ZP_01262138.1 	arginine decarboxylase [Vibrio...	27.8	82
gi 27365676 ref NP_761204.1 	Biosynthetic arginine decarboxyl...	27.8	82
gi 28211946 ref NP_782890.1 	transporter [Clostridium tetani ...	27.8	82
gi 48474851 sp Q8DA54 SPEA_VIBVU	Biosynthetic arginine decarboxy	27.8	82
gi 37680170 ref NP_934779.1 	arginine decarboxylase [Vibrio v...	27.8	82
gi 28900025 ref NP_799680.1 	arginine decarboxylase [Vibrio p...	27.8	82
gi 89097558 ref ZP_01170447.1 	hypothetical protein B14911_28...	27.8	82
gi 116183343 ref ZP_01473359.1 	hypothetical protein VEx2w_02...	27.8	82
gi 125972821 ref YP_001036731.1 	Allergen V5/Tpx-1 related [C...	27.8	82
gi 145603308 ref XP_369328.2 	predicted protein [Magnaporthe ...	27.4	110
gi 34419518 ref NP_899531.1 	conserved hypothetical protein [...	27.4	110
gi 151942736 gb EDN61082.1 	multidrug transporter [Saccharomyces	26.9	148
gi 83643746 ref YP_432181.1 	predicted membrane protein [Hahe...	26.9	148
gi 6325199 ref NP_015267.1 	Pdr12p [Saccharomyces cerevisiae]...	26.9	148
gi 154298886 ref XP_001549864.1 	hypothetical protein BC1G_11...	26.5	198
gi 124901193 gb EAY71943.1 	hypothetical protein BDAG_04799 [Bur	26.5	198
gi 119484721 ref ZP_01619203.1 	hypothetical protein L8106_14...	26.5	198
gi 42524019 ref NP_969399.1 	norD protein [Bdellovibrio bacte...	26.5	198
gi 27377860 ref NP_769389.1 	probable C4-dicarboxylate-bindin...	26.5	198
gi 84358142 ref ZP_00982936.1 	COG0667: Predicted oxidoreduct...	26.5	198
gi 156354066 ref XP_001623224.1 	predicted protein [Nematoste...	26.1	266
gi 150386565 ref ZP_01925098.1 	hypothetical protein VvadDRAF...	26.1	266
gi 116073638 ref ZP_01470900.1 	hypothetical protein RS9916_3...	26.1	266
gi 49881343 gb AAP94609.2 	putative repeating unit transporter [26.1	266
gi 58039122 ref YP_191086.1 	Xanthine dehydrogenase XdhB prot...	26.1	266
gi 83767084 dbj BAE57224.1 	unnamed protein product [Aspergillus	26.1	266
gi 68642382 emb CAI32798.1 	flippase Wzx [Streptococcus pneumoni	26.1	266
gi 71024475 ref XP_762467.1 	hypothetical protein UM06320.1 [...	26.1	266
gi 157337747 emb CAO22093.1 	unnamed protein product [Vitis vini	25.7	356
gi 155966362 gb ABU41133.1 	Sptzle 2-like protein [Lepeophtheiru	25.7	356
gi 147858689 emb CAN78877.1 	hypothetical protein [Vitis vinifer	25.7	356
gi 90416311 ref ZP_01224243.1 	probable lipoprotein signal pe...	25.7	356

gi 109480740 ref XP_216928.4 	PREDICTED: similar to WD repeat do	24.8	642
gi 157127035 ref XP_001654771.1 	conserved hypothetical prote...	24.8	642
gi 108756771 ref YP_634100.1 	hypothetical protein MXAN_5965 ...	24.8	642
gi 86564650 ref NP_001033528.1 	C25F6.8 [Caenorhabditis elega...	24.8	642
gi 73975339 ref XP_539290.2 	PREDICTED: similar to Signal-tra...	24.8	642
gi 88800179 ref ZP_01115747.1 	predicted membrane protein [Re...	24.8	642

Alignments

>[gi|15614366|ref|NP_242669.1|](#)  hypothetical protein BH1803 [Bacillus halodurans
[gi|10174421|dbj|BAB05522.1|](#)  BH1803 [Bacillus halodurans C-125]
Length=207

Score = 31.6 bits (67), Expect = 5.8
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 4    HYWTQMF 10
          HYWTQMF
Sbjct 198  HYWTQMF 204

```


>[gi|89097516|ref|ZP_01170405.1|](#) hypothetical protein B14911_27995 [Bacillus sp. N
[gi|89087812|gb|EAR66924.1|](#) hypothetical protein B14911_27995 [Bacillus sp. NRRL
Length=207

Score = 31.6 bits (67), Expect = 5.8
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 4    HYWTQMF 10
          HYWTQMF
Sbjct 198  HYWTQMF 204

```



>[gi|46139389|ref|XP_391385.1|](#)  hypothetical protein FG11209.1 [Gibberella zeae P
Length=897

Score = 30.8 bits (65), Expect = 10
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

```

Query 4    HYWTQMFY 11
          HYWT MFY
Sbjct 225  HYWTMMFY 232

```

>[gi|23098322|ref|NP_691788.1|](#)  hypothetical protein OB0867 [Oceanobacillus ihey
[gi|22776548|dbj|BAC12823.1|](#)  hypothetical conserved protein [Oceanobacillus ihe
Length=278

Score = 29.5 bits (62), Expect = 25
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

```

Query 2    HV---HYWTQMF 10
          HV   +YWTQMF
Sbjct 264  HVENGNYWTQMF 275

```

>[gi|89097846|ref|ZP_01170733.1|](#) YkwD [Bacillus sp. NRRL B-14911]
[gi|89087348|gb|EAR66462.1|](#) YkwD [Bacillus sp. NRRL B-14911]
Length=258

Score = 29.5 bits (62), Expect = 25
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

```

Query 2    HV---HYWTQMF 10
          HV   +YWTQMF



```

Distance tree of results NEW

Sequences producing significant alignments:		Score (Bits)	E Value
gi 23098322 ref NP_691788.1 	hypothetical protein OB0867 [Oce...	29.9	19
gi 146296177 ref YP_001179948.1 	Allergen V5/Tpx-1 family pro...	28.6	46
gi 66804519 ref XP_635992.1 	hypothetical protein DDBDRAFT_01...	28.6	46
gi 15614366 ref NP_242669.1 	hypothetical protein BH1803 [Bac...	28.2	61
gi 89097516 ref ZP_01170405.1 	hypothetical protein B14911_27...	28.2	61
gi 89097846 ref ZP_01170733.1 	Ykwd [Bacillus sp. NRRL B-1491...	28.2	61
gi 153940849 ref YP_001391336.1 	SCP-like extracellular prote...	27.8	82
gi 149181592 ref ZP_01860086.1 	hypothetical protein BSG1_137...	27.8	82
gi 149179719 ref ZP_01858224.1 	hypothetical protein BSG1_018...	27.8	82
gi 149182265 ref ZP_01860745.1 	hypothetical protein BSG1_199...	27.8	82
gi 148379973 ref YP_001254514.1 	exported protein [Clostridiu...	27.8	82
gi 126651239 ref ZP_01723449.1 	hypothetical protein BB14905_...	27.8	82
gi 118081874 ref XP_415358.2 	PREDICTED: similar to SBF1 protein	27.8	82
gi 28211946 ref NP_782890.1 	transporter [Clostridium tetani ...	27.8	82
gi 13507984 ref NP_109933.1 	peptide deformylase [Mycoplasma ...	27.8	82
gi 89097558 ref ZP_01170447.1 	hypothetical protein B14911_28...	27.8	82
gi 125972821 ref YP_001036731.1 	Allergen V5/Tpx-1 related [C...	27.8	82
gi 34419518 ref NP_899531.1 	conserved hypothetical protein [...	27.4	110
gi 46139389 ref XP_391385.1 	hypothetical protein FG11209.1 [Gib	27.4	110
gi 31239659 ref XP_320243.1 	ENSANGP00000024642 [Anopheles ga...	27.4	110
gi 83643746 ref YP_432181.1 	predicted membrane protein [Hahe...	26.9	148
gi 156399682 ref XP_001638630.1 	predicted protein [Nematoste...	26.5	198
gi 113681530 ref NP_001038623.1 	SET binding factor 1 [Danio ...	26.5	198
gi 20026648 ref NP_612690.1 	tegument protein UL47 [Chimpanze...	26.5	198
gi 71282430 ref YP_269817.1 	hypothetical protein CPS_3120 [C...	26.5	198
gi 27377860 ref NP_769389.1 	probable C4-dicarboxylate-bindin...	26.5	198
gi 150386565 ref ZP_01925098.1 	hypothetical protein VvadDRAF...	26.1	266
gi 150384287 ref ZP_01922988.1 	hypothetical protein VvadDRAF...	26.1	266
gi 78127855 gb ABB22239.1 	thymidine kinase-like protein [Ovine	26.1	266
gi 29830538 ref NP_825172.1 	hypothetical protein SAV3995 [St...	26.1	266
gi 83642858 ref YP_438145.1 	ORF21 [Ovine herpesvirus 2] >gi ...	26.1	266
gi 157018437 gb EAL41048.3 	AGAP010349-PA [Anopheles gambiae str	25.7	356
gi 156546066 ref XP_001600764.1 	PREDICTED: similar to conser...	25.7	356
gi 155368551 emb CAM98568.1 	NADH4 protein [Ailuropoda melanoleu	25.7	356
gi 151942736 gb EDN61082.1 	multidrug transporter [Saccharomyces	25.7	356
gi 148298641 ref YP_001249293.1 	NADH dehydrogenase subunit 4...	25.7	356
gi 148980161 ref ZP_01815912.1 	hypothetical protein VSWAT3_1...	25.7	356
gi 119622541 gb EAX02136.1 	protein regulator of cytokinesis ...	25.7	356
gi 119859347 ref ZP_01640763.1 	peptidase S9, prolyl oligopep...	25.7	356
gi 116668578 ref YP_829511.1 	glycosyl transferase, family 2 ...	25.7	356
gi 118781666 ref XP_559110.2 	ENSANGP00000027759 [Anopheles gamb	25.7	356
gi 115494701 ref YP_778730.1 	NADH dehydrogenase subunit 4 [P...	25.7	356
gi 114659016 ref XP_510600.2 	PREDICTED: protein regulator of cy	25.7	356
gi 110778133 ref XP_623923.2 	PREDICTED: similar to CG32415-PA [25.7	356
gi 109082407 ref XP_001098763.1 	PREDICTED: similar to protei...	25.7	356


gi 154303054 ref XP_001551935.1 	predicted protein [Botryotin...	24.8	642
gi 154276406 ref XP_001539048.1 	predicted protein [Ajellomyc...	24.8	642
gi 154277792 ref XP_001539729.1 	predicted protein [Ajellomyc...	24.8	642
gi 145547645 ref XP_001459504.1 	hypothetical protein [Parame...	24.8	642
gi 145495780 ref XP_001433882.1 	hypothetical protein [Parame...	24.8	642
gi 145480331 ref XP_001426188.1 	hypothetical protein [Parame...	24.8	642
gi 145480543 ref XP_001426294.1 	hypothetical protein [Parame...	24.8	642
gi 145475379 ref XP_001423712.1 	hypothetical protein [Parame...	24.8	642


Alignments

>[gi|23098322|ref|NP_691788.1|](#)  hypothetical protein OB0867 [Oceanobacillus iheye
[gi|22776548|dbj|BAC12823.1|](#)  hypothetical conserved protein [Oceanobacillus ihe
Length=278

Score = 29.9 bits (63), Expect = 19
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)


```
Query 2   HVQ---YWTQMF 10
          HV+   YWTQMF
Sbjct 264 HVENGNYWTQMF 275
```


>[gi|146296177|ref|YP_001179948.1|](#)  Allergen V5/Tpx-1 family protein [Caldicellu
DSM 8903]

[gi|145409753|gb|ABP66757.1|](#)  Allergen V5/Tpx-1 family protein [Caldicellulosir
DSM 8903]
Length=203

Score = 28.6 bits (60), Expect = 46
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)



```
Query 3   VQYWTQMF 10
          V YWTQMF
Sbjct 192 VLYWTQMF 199
```

>[gi|66804519|ref|XP_635992.1|](#)  hypothetical protein DDBDRAFT_0188654 [Dictyostel
AX4]

[gi|60464332|gb|EAL62481.1|](#)  hypothetical protein DDBDRAFT_0188654 [Dictyosteliu
AX4]
Length=871

Score = 28.6 bits (60), Expect = 46
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

```
Query 4   QYWTQMFY 11
          QYW +MFY
Sbjct 247 QYWNEMFY 254
```

>[gi|15614366|ref|NP_242669.1|](#)  hypothetical protein BH1803 [Bacillus halodurans
[gi|10174421|dbj|BAB05522.1|](#)  BH1803 [Bacillus halodurans C-125]
Length=207

Score = 28.2 bits (59), Expect = 61
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

```
Query 4   QYWTQMF 10
          YWTQMF
Sbjct 198 HYWTQMF 204
```